Please amend the specification by inserting the following replacement paragraphs:

Please replace the paragraph at page 1, line 17 through page 2, line 2, with the following paragraph:

Sequence tagged connectors, or STCs, are sequences of insert data generated from both ends (at the vector-insert point) of a BAC clone in a genomic library. These sequences, and BACs containing these STC sequences, can be used, for example, for marker development, genetic mapping or linkage analysis, marker assisted breeding, and physical genome mapping (Venter, *et al., Nature, 381:*364-366 (1996), the entirety of which is herein incorporated by reference; Choi and Wing, available on the world wide web at: genome.clemson.edu/protocols2-nj.html July, 1998). STCs can represent a copy of up to a full length of a mRNA transcript, a promoter element or part of a promoter, can contain simple sequence repeats (also called microsatellites) repetitive elements or fragments of repetitive elements, other DNA markers, or any combination thereof.

Please replace the paragraph at page at page 4, line 20 to page 5, line 7 with the following paragraph:

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ), accessible on the world wide web at ddbj.nig.ac.jp/); Genebank, accessible on the world wide web at ncbi.nlm.nih.gov/web/Genbank/Index.html); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL), accessible on the world wide web at ebi.ac.us/ebi_docs/embl_db.html). A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for

protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology, 12*:76-80 (1994); Birren, *et al., Genome Analysis, 1*:543-559 (1997)).

Please replace the paragraph at page Page 24, lines 8-14 with the following paragraph:

Genomic sequences can be screened for the presence of proteins or genes utilizing one or a number of different search algorithms have that been developed, one example of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background and under the section titled "Uses of the Agents of the Invention." In addition, unidentified reading frames may be screened for protein coding regions by prediction software such as GenScan, which is located on the world wide web at gnomic.stanford.edu/GENSCANW.html.

Please replace the paragraphs at page 96, lines 9 to page 97, line 8 with the following paragraphs:

Primers are designed from good quality unique sequences. A public available primer software program, PRIMER 3, (Cambridge, MA) is used. PRIMER 3 can be accessed through the internet wi.mit.edu/cgi-bin/primer/primer3.cgi. Default parameters are used except for those product size primer size changed. Product size is Min: 80, Opt: 100, Max 120, while Primer Size is Min: 18, Opt. 22 and Max 27. Oligos are synthesized by Genosis Biotechnologies, Inc. Houston, Texas).

The above protocols are used to develop primers from Sequence id GM_M02_A2_B07_MR_MR containing the following nucleotide composition:

AGGCGTTTTNCCTTGATACCTTCGNAGGTCCANCCTTTTNCTTGCTGTATCGACTCAT

TAACACCAAGCTCGGTGAGCACTCTGAAGATTATGACAACTTTCGNTGATCTTTTTG

TCATCGATATTNTAGNAGAGACCAATCTTTCTTCTTCAAATGTCGCTCATGATATTTA